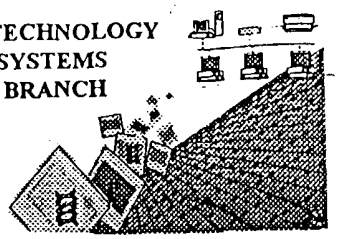
BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/789,494
Source: FWO
Date Processed by STIC: 8/25/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):** U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

IFWO

RAW SEQUENCE LISTING DATE: 08/25/2004
PATENT APPLICATION: **US/10/789,494** TIME: 15:48:49

Input Set : **A:\PTO.FG.txt**
Output Set: **N:\CRF4\08252004\J789494.raw**

2 <110> APPLICANT: TSUBOUCHI, Kozo
3 YAMADA, Hiromi
5 <120> TITLE OF INVENTION: EXTRACTION AND UTILIZATION OF CELL
6 GROWTH-PROMOTING PEPTIDES FROM SILK PROTEIN
8 <130> FILE REFERENCE: OPS 635
C--> 10 **<140> CURRENT APPLICATION NUMBER: US/10/789,494**
11 <141> CURRENT FILING DATE: 2004-02-27
13 <150> PRIOR APPLICATION NUMBER: JP 2003-55048
14 <151> PRIOR FILING DATE: 2003-02-28
E--> 16 **<160> NUMBER OF SEQ ID NOS:** 68 - Found 85

ERRORED SEQUENCES

Does Not Comply
Corrected Diskette Needed
(pg. 1-7)

18 <210> SEQ ID NO: 1
19 <211> LENGTH: 10
20 <212> TYPE: PRT
21 <213> ORGANISM: Bombyx mori
23 <220> FEATURE:
25 <400> SEQUENCE: 1
26 Val Ile Thr Thr Asp Ser Asp Gly Asn Glu
E--> 27 5 10 5 10
29 <210> SEQ ID NO: 2
30 <211> LENGTH: 8
31 <212> TYPE: PRT
32 <213> ORGANISM: Bombyx mori
34 <220> FEATURE:
36 <400> SEQUENCE: 2
37 Asn Ile Asn Asp Phe Asp Glu Asp
E--> 38 5 5
78 <210> SEQ ID NO: 6
79 <211> LENGTH: 6
80 <212> TYPE: PRT
81 <213> ORGANISM: Antheraea yamamai
83 <220> FEATURE:
85 <400> SEQUENCE: 6
86 Asp Glu Tyr Val Asp Asn
E--> 87 5 5
102 <210> SEQ ID NO: 8
103 <211> LENGTH: 13
104 <212> TYPE: PRT
105 <213> ORGANISM: Antheraea yamamai
107 <220> FEATURE:

RAW SEQUENCE LISTING DATE: 08/25/2004
PATENT APPLICATION: **US/10/789,494** TIME: 15:48:49

Input Set : **A:\PTO.FG.txt**
Output Set: **N:\CRF4\08252004\J789494.raw**

```
    109 <400> SEQUENCE: 8
    110 Asp Asp Gly Phe Val Leu Asp Gly Gly Tyr
E--> 111     5    10                   5                  10
    112 Asp Ser Glu
    320 <210> SEQ ID NO: 22
    321 <211> LENGTH: 262
    322 <212> TYPE: PRT
    323 <213> ORGANISM: Bombyx mori
    325 <220> FEATURE:
    327 <400> SEQUENCE: 22
    328 Met Lys Pro Ile Phe Leu Val Leu Leu Val Ala Thr Ser Ala
    329                 5                  10
    330 Tyr Ala Ala Pro Ser Val Thr Ile Asn Gln Tyr Ser Asp Asn
    331 15                  20                  25
    332 Glu Ile Pro Arg Asp Ile Asp Asp Gly Lys Ala Ser Ser Val
    333     30                  35                  40
    334 Ile Ser Arg Ala Trp Asp Tyr Val Asp Asp Thr Asp Lys Ser
    335         45                  50                  55
    336 Ile Ala Ile Leu Asn Val Gln Glu Ile Leu Lys Asp Met Ala
    337             60                  65                  70
    338 Ser Gln Gly Asp Tyr Ala Ser Gln Ala Ser Ser Val Ala Gln
    339                 75                  80
    340 Thr Ala Gly Ile Ile Ala His Leu Ser Ala Gly Ile Pro Gly
    341 85                  90                  95
    342 Asp Ala Cys Ala Ala Ala Asn Val Ile Asn Ser Tyr Thr Asp
    343     100                 105                 110
    344 Gly Val Arg Ser Gly Asn Phe Ala Gly Phe Arg Gln Ser Leu
    345         115                 120                 125
    346 Gly Pro Phe Phe Gly His Val Gly Gln Asn Leu Asn Leu Ile
    347             130                 135                 140
    348 Asn Gln Leu Val Ile Asn Pro Gly Gln Leu Arg Tyr Ser Val
    349                 145                 150
    350 Gly Pro Ala Leu Gly Cys Ala Gly Gly Gly Arg Ile Tyr Asp
    351 155                 160                 165
    352 Phe Glu Ala Ala Trp Asp Ala Ile Leu Ala Ser Ser Asp Ser
    353     170                 175                 180
    354 Ser Phe Leu Asn Glu Glu Tyr Cys Ile Val Lys Arg Leu Tyr
    355         185                 190                 195
    356 Asn Ser Arg Asn Ser Gln Ser Asn Asn Ile Ala Ala Tyr Ile
    357             200                 205                 210
    358 Thr Ala His Leu Leu Pro Pro Val Ala Gln Val Phe His Gln
    359                 215                 220
    360 Ser Ala Gly Ser Ile Thr Asp Leu Leu Arg Gly Val Gly Asn
    361 225                 230                 235
    362 Gly Asn Asp Ala Thr Gly Leu Val Ala Asn Ala Gln Arg Tyr
    363     240                 245                 250
E--> 364 Ile Ala Gln Alg Ala Ser Gln Val His Val
    365         255                 260
    602 <210> SEQ ID NO: 40
```

Invalid Amino acid designator

RAW SEQUENCE LISTING DATE: 08/25/2004
PATENT APPLICATION: US/10/789,494 TIME: 15:48:49

Input Set : A:\PTO.FG.txt
Output Set: N:\CRF4\08252004\J789494.raw

603 <211> LENGTH: 22
604 <212> TYPE: PRT
605 <213> ORGANISM: Antheraea yamamai
607 <220> FEATURE:
E--> 611 <400> SEQUENCE: <400> 40 <4007
612 Gly Ser Gly Ala Gly Gly Val Gly Gly Gly Tyr Gly Trp Gly
613 5 10
614 Asp Gly Gly Tyr Gly Ser Asp Ser
615 15 20
693 <210> SEQ ID NO: 47
694 <211> LENGTH: 15
E--> 695 <212> TYPE: 16 - Invalid Response, <212> (response) has to be either DNA/RNA or PRT.
696 <213> ORGANISM: Antheraea yamamai
698 <220> FEATURE:
700 <400> SEQUENCE: 47
701 Ser Gly Ala Gly Gly Ser Gly Gly Tyr Gly Gly Tyr Gly Ser
702 5 10
703 Asp Ser
704 15
706 <210> SEQ ID NO: 48
707 <211> LENGTH: 25
708 <212> TYPE: PRT
709 <213> ORGANISM: Antheraea yamamai
711 <220> FEATURE:
E--> 713 <400> SEQUENCE: <400> 48 <4007
714 Gly Ser Gly Ala Gly Gly Val Gly Gly Gly Tyr Gly Trp Gly
715 5 10
716 Asp Gly Gly Tyr Gly Gly Tyr Gly Ser Asp Ser
717 15 20 25
743 <210> SEQ ID NO: 51
744 <211> LENGTH: 21
745 <212> TYPE: PRT
746 <213> ORGANISM: Antheraea yamamai
748 <220> FEATURE:
750 <400> SEQUENCE: 51 - Invalid Amino Acid designator
E--> 751 Ser Gly Ala Gyl Gly Ser Gly Gly Gly Tyr Gly Trp Asp Tyr
752 5 10
753 Gly Ser Tyr Gly Ser Asp Ser
754 15 20
756 <210> SEQ ID NO: 52
757 <211> LENGTH: 22
758 <212> TYPE: PRT
759 <213> ORGANISM: Antheraea yamamai
761 <220> FEATURE:
E--> 763 <400> SEQUENCE: <400> 52 <4007
764 Ser Ser Gly Ala Gly Gly Ser Gly Gly Gly Tyr Gly Trp Asp
765 5 10
766 Tyr Gly Gly Tyr Gly Ser Asp Ser
767 15 20

RAW SEQUENCE LISTING DATE: 08/25/2004
PATENT APPLICATION: **US/10/789,494** TIME: 15:48:49

Input Set : **A:\PTO.FG.txt**
Output Set: **N:\CRF4\08252004\J789494.raw**

782 <210> SEQ ID NO: 54
783 <211> LENGTH: 14
784 <212> TYPE: PRT
785 <213> ORGANISM: Antheraea yamamai
787 <220> FEATURE:
789 <400> SEQUENCE: 54
E--> 790 **Ser Arg Arg Ala Gly His Asp Arg Ala Try Gly Ala Gly Ser**
791 5 10

Invalid Amino Acid designator

<210> 78
<211> 4
<212> PRT
<213> Artificial sequence

Leave blank

<220> Cell growth promoting activity

<223>

Insert this response beside numeric identifier <223>.

<400> 78
Glu Glu Glu Glu

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

<210> 85
<211> 4
<212> PRT
<213> Artificial sequence

leave blank

<220> Cell growth promoting activity

<223>

insert beside <223>.

<400> 85
Tyr Tyr Tyr Tyr

delete

1

VERIFICATION SUMMARY DATE: 08/25/2004
PATENT APPLICATION: **US/10/789,494** TIME: 15:48:50

Input Set : **A:\PTO.FG.txt**
Output Set: **N:\CRF4\08252004\J789494.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:27 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:38 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:87 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
L:111 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:364 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:611 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:40 differs:39
L:695 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:713 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:48 differs:47
L:751 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:763 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:52 differs:51
L:790 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:1078 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:1080 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:78, <213>
ORGANISM:Artificial sequence
L:1080 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:78,Line#:1080
L:1088 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:1092 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:79, <213>
ORGANISM:Artificial sequence
L:1092 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:79,Line#:1092
L:1101 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:1103 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:80, <213>
ORGANISM:Artificial sequence
L:1103 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:80,Line#:1103
L:1112 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:1114 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:81, <213>
ORGANISM:Artificial sequence
L:1114 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:81,Line#:1114
L:1123 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:1127 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:82, <213>
ORGANISM:Artificial sequence
L:1127 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:82,Line#:1127
L:1136 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:1138 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:83, <213>
ORGANISM:Artificial sequence
L:1138 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:83,Line#:1138
L:1147 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:1149 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:84, <213>
ORGANISM:Artificial sequence
L:1149 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:84,Line#:1149
L:1158 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:1161 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:85, <213>
ORGANISM:Artificial sequence
L:1161 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:85,Line#:1161
L:16 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (68) Counted (85)